

PCT10

RAW SEQUENCE LISTING DATE: 05/15/2002
PATENT APPLICATION: US/10/019,676 TIME: 16:03:22

Input Set : A:\EP.txt

Output Set: N:\CRF3\05152002\J019676.raw

ENTERED

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3 <110> APPLICANT: Li, Sam Fong Yau
              Su, Xiaodi
      5
              Kwang, Jimmy
              Low, Sharon
              Liu, Wei
              Institute of Molecular Agrobiology
     10 <120> TITLE OF INVENTION: A NOVEL IMMUNO-DIAGNOSTIC TEST METHOD FOR VETERINARY
              DISEASE
     13 <130> FILE REFERENCE: GM/MC/R33-77
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/019,676
C--> 16 <141> CURRENT FILING DATE: 2002-04-24
     18 <150> PRIOR APPLICATION NUMBER: SG 9903147-8
     19 <151> PRIOR FILING DATE: 1999-07-05
     21 <160> NUMBER OF SEQ ID NOS: 4
     23 <170> SOFTWARE: PatentIn Ver. 2.0
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 270
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Salmonella enteritidis
     30 <220> FEATURE:
     31 <221> NAME/KEY: CDS
     32 <222> LOCATION: (1)..(270)
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     36 Ser Thr Ala Gly Thr Ala Glu Ala Lys Ala Ile Ala Gly Ala Ile Lys
     37
     39 ggt ggt aag gaa gga gat acc ttt gat tat aaa ggc gtg act ttt act
     40 Gly Gly Lys Glu Gly Asp Thr Phe Asp Tyr Lys Gly Val Thr Phe Thr
     43 att gat aca aaa act ggt gat gac ggt aat ggt aag gtt tct act acc
                                                                            144
     44 Ile Asp Thr Lys Thr Gly Asp Asp Gly Asn Gly Lys Val Ser Thr Thr
                 35
                                     40
                                                          45
    45
     49 atc aat ggt gaa aaa gtt acg tta act gtc gct gat att gcc act ggc
                                                                            192
     50 Ile Asn Gly Glu Lys Val Thr Leu Thr Val Ala Asp Ile Ala Thr Gly
                                 55
     53 gcg acg gat gtt aat gct gct acc tta caa tca agc aaa aat gtt tat
                                                                            240
     54 Ala Thr Asp Val Asn Ala Ala Thr Leu Gln Ser Ser Lys Asn Val Tyr
                             70
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     57 aca tct gta gtg aac ggt cag ttt act ttt
     58 Thr Ser Val Val Asn Gly Gln Phe Thr Phe
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    62 <210> SEQ ID NO: 2
     63 <211> LENGTH: 90
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65 <213> ORGANISM: Salmonella enteritidis
67 <400> SEQUENCE: 2
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71 Gly Gly Lys Glu Gly Asp Thr Phe Asp Tyr Lys Gly Val Thr Phe Thr
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74 Ile Asp Thr Lys Thr Gly Asp Asp Gly Asn Gly Lys Val Ser Thr Thr
            35
                                40
77 Ile Asn Gly Glu Lys Val Thr Leu Thr Val Ala Asp Ile Ala Thr Gly
80 Ala Thr Asp Val Asn Ala Ala Thr Leu Gln Ser Ser Lys Asn Val Tyr
81 65
                        70
83 Thr Ser Val Val Asn Gly Gln Phe Thr Phe
84
                    85
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 630
89 <212> TYPE: DNA
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92 <220> FEATURE:
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94 <222> LOCATION: (1)..(600)
96 <400> SEQUENCE: 3
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98 Met Leu Gly Lys Cys Leu Thr Val Gly Cys Cys Ser Arg Leu Leu Ser
99
                                        10
101 ttg tgg tgt atc gtg ccg ttc tgt ttt gct gtg ctc gcc gac gcc cac
                                                                        96
102 Leu Trp Cys Ile Val Pro Phe Cys Phe Ala Val Leu Ala Asp Ala His
103
                                     25
105 age age age tet eat etg caa tte att tae aac ttg aeg eta tgt
                                                                       144
106 Ser Ser Ser Ser His Leu Gln Phe Ile Tyr Asn Leu Thr Leu Cys
107
             35
                                 40
                                                                       192
109 gag ctg aat ggc aca gat tgg cta gct gat aga ttt gat tgg gca gtg
110 Glu Leu Asn Gly Thr Asp Trp Leu Ala Asp Arg Phe Asp Trp Ala Val
111
         50
113 gag age ttt gtc atc ttt cct gtt ttg act cac att gtc tcc tat ggt
                                                                       240
114 Glu Ser Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly
                         70
                                             75
117 gcc ctc act acc agc cat ttc ctt gac aca att gct tta gtc act gtg
                                                                       288
118 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Ile Ala Leu Val Thr Val
119
                     85
121 tot acc gcc ggg ttt gtt cac ggg cgg tat gtc ctg agt agc atc tac
                                                                       336
122 Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Ile Tyr
                100
                                    105
                                                         110
125 gcg gtc tqt gcc ctg gct gcg ttg act tqc ttc gtc att agg ttt gta
                                                                       384
126 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Arg Phe Val
            115
                                120
                                                    125
129 aag aat tgc atg tcc tgg cgc tac tca tgt act aga tat acc aac ttt
                                                                       432
130 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe
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133 ctt ctg gac act aag ggc aga ctc tat cgt tgg cgg tcg cct gtc att 134 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val I1e 135 145 137 ata gag aag agg ggc aaa gtt gag gtc gaa ggt cat ctg atc gat ctc 138 I1e Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu I1e Asp Leu 139 165 170 175 180 180 181 182 183 181 e Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu I1e Asp Leu 139 165 170 175 181 182 183 184 185 186 187 188 188 188 188 188 188 188 188 188	131		130					135					140					
134 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 135 145 150 150 155 160 160 161 160 153 145 160 155 160 160 153 165 160 175 160 175 160 175 160 175 160 175 175 175 175 170 175		att		720	ant	220	aac		ata	tat	cat	taa		ton	cct	ata	2++	480
135																		400
137 ata gag aag agg ggc aaa gtt gag gtc gaa ggt cat ctg atc gat ctc 138 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu 139 165 141 aaa aga gtt gtg ctt gat ggt tcc gtg gca acc cct ata acc aga gtt 141 aaa aga gtt gtg ctt gat ggt tcc gtg gca acc cct ata acc aga gtt 142 Lys Arg Val Val Leu Asp Gly Ser Val Ala Thr Pro Ile Thr Arg Val 143 180 190 145 tca gcg gaa caa tgg ggt cgt cat tagatgactt ctgtcatgat agcacggctc 630 146 Ser Ala Glu Gln Trp Gly Arg His 147 195 200 150 <210> SEQ ID NO: 4 151 <211> LENGTH: 200 152 <212> TYPE: PRT 153 <213> ORGANISM: Porcine reproductive and respiratory syndrome virus 155 <400> SEQUENCE: 4 156 Met Leu Gly Lys Cys Leu Thr Val Gly Cys Cys Ser Arg Leu Leu Ser 157 1 5 1 5 30 162 Ser Ser Ser Ser His Leu Gln Phe Ile Tyr Asn Leu Thr Leu Cys 163 35 40 164 Glu Leu Asn Gly Thr Asp Trp Leu Ala Asp Arg Phe Asp Trp Ala Val 166 50 5 60 168 Glu Ser Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly 169 65 70 75 80 171 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Ile Ala Leu Val Thr Val 172 85 90 174 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Asp Phe Val 175 100 105 176 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Arg Phe Val 177 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Arg Phe Val 178 115 180 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe 181 130 135 140 183 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 184 145 150 160			пеп	изр	1111	цуз		пту	пси	1 7 1	Arg		nra	JCI	110	Vul		
138			a a a	220	200	ααα	-	att	man.	atc	maa		cat	cta	ato	a t		528
165																		320
141 aaa aga gtt gtg ctt gat ggt tcc gtg gca acc cct ata acc aga gtt 576 142 Lys Arg Val Val Leu Asp Gly Ser Val Ala Thr Pro Ile Thr Arg Val 143		116	Giu	Буз	nr 9		цуэ	vai	Giu	vai		Gry	1113	пси	110		Deu	
142 Lys Arg Val Val Leu Asp Gly Ser Val Ala Thr Pro Ile Thr Arg Val 143		222	ада	att	ata		αat	aat	tcc	ata		acc	cct	ata	acc		att	576
143																		3,0
145 tca gcg gaa caa tgg ggt cgt cat tagatgactt ctgtcatgat agcacggctc 630 146 Ser Ala Glu Gln Trp Gly Arg His 147		Lys	1119	vai		DCu	шор	011	UCI		1114			110		*** 9	, 42	
146 Ser Ala Glu Gln Trp Gly Arg His 147		t.ca	aca	σаа		t.aa	aat.	cat.	cat.		atga	ett o	ctato	cato		rcaco	actc	630
147				-				-								,	,,	
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157	155	<400)> SI	EQUE	NCE:	4		-										
159 Leu Trp Cys Ile Val Pro Phe Cys Phe Ala Val Leu Ala Asp Ala His 160	15.6	Met	Leu	Gly	Lys	Cys	Leu	Thr	Val	Gly	Cys	Cys	Ser	Arg	Leu	Leu	Ser	
160	157	1		_	_	5					10					15		
162 Ser Ser Ser Ser Ser Ser His Leu Gln Phe Ile Tyr Asn Leu Thr Leu Cys 163	159	Leu	Trp	Cys	Ile	Val	Pro	Phe	Cys	Phe	Ala	Val	Leu	Ala	Asp	Ala	His	
163 35 40 40 Asp Gly Thr Asp Trp Leu Ala Asp Trp Leu Ala Asp Trp Gly For Strp For	160				20					25					30			
165 Glu Leu Asn Gly Thr Asp Trp Leu Ala Asp Arg Phe Asp Trp Ala Val 166 50 50 55 60 168 Glu Ser Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly 169 65 70 70 75 80 171 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Ile Ala Leu Val Thr Val 172 85 90 95 174 Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Ile Tyr 175 100 105 105 110 177 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Arg Phe Val 178 115 20 120 125 180 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe 181 130 135 120 140 183 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 184 145 150 150 160 186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu	162	Ser	Ser	Ser	Ser	Ser	His	Leu	Gln	Phe	Ile	Tyr	Asn	Leu	Thr	Leu	Cys	
166 50 55 60 168 Glu Ser Phe Val Ile Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly 75 80 169 65 70 70 75 75 80 171 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Ile Ala Leu Val Thr Val 90 95 95 174 Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Ile Tyr 100 100 105 110 177 Ala Val Cys Ala Leu Ala Ala Leu Ala Leu Thr Cys Phe Val Ile Arg Phe Val 178 120 125 180 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe 135 140 181 130 135 135 140 183 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Trp Arg Ser Pro Val Ile 160 160 184 145 150 155 160 186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu	163			35					40					45				
168 Glu Ser Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly 169 65	165	Glu	Leu	Asn	Gly	Thr	Asp	Trp	Leu	Ala	Asp	Arg	Phe	Asp	\mathtt{Trp}	Ala	Val	
169 65 70 75 80 171 Ala Leu Thr Thr Ser His Phe Leu Asp Thr Ile Ala Leu Val Thr Val 85 90 174 186 186 90 95 95 95 95 180 174 185 180 </td <td></td>																		
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172		-		_	_								_		_			
174 Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Ile Tyr 175		Ala	Leu	Thr	Thr		His	Phe	Leu	Asp		Ile	Ala	Leu	Val		Val	
175 100 105 105 110		_	1				1			_			_	_	_		_	
177 Ala Val Cys Ala Leu Ala Ala Leu Thr Cys Phe Val Ile Arg Phe Val 178		Ser	Thr	Ala	_	Phe	Vai	His	GTA		Tyr	vaı	Leu	Ser		тте	Tyr	
178 115 120 125 180 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe 181 130 135 135 140 140 150 150 150 Trp Arg Trp Arg Ser Pro Val Ile 184 145 150 150 155 160 160 186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu His Leu Ile Asp Leu			**- 1	a					T		G	Db.	77- 1	-1 -		Dh.	17 1	
180 Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Arg Tyr Tyr Arg Tyr Tyr Arg Ser Pro Val Ile 184 145 150 155 160 186 Ile Glu Lys Arg Glu Val Glu Glu His Leu Ile Asp Leu		Ата	vaı	_	Ата	ьеи	Ата	Ата		Thr	Cys	ьие	Val		Arg	Pne	vaı	
181 130 135 140 183 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 184 145 150 155 160 186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu		T	3		16-±	a	m	3		C	O	mbs	A		mh m	7	Dho	
183 Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile 184 145		гаг		Cys	met	ser	тгр	_	TAL	ser	Cys	THE		TAT	THE	ASII	Pile	
184 145 150 155 160 186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu		Tou		λan	mb r	Two	C111		T 011	Titto	λκα	Trn		Sor	Dro	V = 1	T10	
186 Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu			ьец	кор	1111	пÃ2	_	AIG	ьец	TAT	Arg	_	Ary	261	PIO	Val		
			C3 n	T.ve	λνα	Glv		Va l	Glu	Va 1	Glu		ніс	T.en	Tla	Δen		
		116	GIU	шуз	лгу	-	цуз	vai	GIU	VUI		Gry	111.5	neu	116		пец	
189 Lys Arg Val Val Leu Asp Gly Ser Val Ala Thr Pro Ile Thr Arg Val		T.ve	Ara	Va 1	Va 1		Asn	G1v	Ser	Va 1		Thr	Pro	Tle	Thr		Val	
190 180 185 190		~10	9	7 44 24		20u		1								9		
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193 195 200						r	1	5										

VERIFICATION SUMMARY

DATE: 05/15/2002

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date